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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

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Reviewer: markspencer

Timestamp: [year=2008; month=5; day=2; hr=15; min=36; sec=47; ms=445; ]

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Reviewer Comments:

Remove the "10" at the end of the file after SEQ ID # 22. Also remove  
the blank <223> in SEQ ID # 1 and 3.

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Application No: 10573478 Version No: 2.0

Input Set:

Output Set:

Started: 2008-04-17 15:51:24.767  
Finished: 2008-04-17 15:51:28.390  
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 623 ms  
Total Warnings: 6  
Total Errors: 4  
No. of SeqIDs Defined: 22  
Actual SeqID Count: 22

Error code	Error Description
E 201	Mandatory field data missing in <223> in SEQ ID (1)
E 201	Mandatory field data missing in <223> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
E 355	Empty lines found between the amino acid numbering and the
E 321	No. of Bases conflict, this line has no nucleotides SEQID (22)

# SEQUENCE LISTING

<110> Kiselev, Vsevolod I  
Petr, Sveshnikov G

<120> METHODS, KITS, AND COMPOSITIONS FOR THE DEVELOPMENT AND USE  
OF MONOCLONAL ANTIBODIES SPECIFIC TO ANTIGENS TRADITIONALLY  
OF LOW IMMUNOGENICITY

<130> Immunize

<140> 10573478

<141> 2008-04-17

<150> RU 2003128660

<151> 2003-09-25

<160> 22

<170> Patentln version 3.1

<210> 1

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<212> DNA

<213> Human papillomavirus type 16

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<221> CDS

<222> (7)..(303)

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Asp Leu Gln Pro Glu Thr Thr Asp Leu Tyr Cys Tyr Glu Gln Leu Asn  
15 20 25 30

gac agc tca gag gag gag gat gaa ata gat ggt cca gct gga caa gca 144  
Asp Ser Ser Glu Glu Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln Ala  
35 40 45

gaa ccg gac aga gcc cat tac aat att gta acc ttt tgt tgc aag tgt 192  
Glu Pro Asp Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys  
50 55 60

gac tct acg ctt cgg ttg tgc gta caa agc aca cac gta gac att cgt 240  
Asp Ser Thr Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile Arg  
65 70 75

act ttg gaa gac ctg tta atg ggc aca cta gga att gtg tgc ccc atc 288  
Thr Leu Glu Asp Leu Leu Met Gly Thr Leu Gly Ile Val Cys Pro Ile  
80 85 90

tgt tct cag aaa cca ggatcc 309  
Cys Ser Gln Lys Pro  
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Ser Glu Glu Glu Asp Glu Ile Asp Gly Pro Ala Gly Gln Ala Glu Pro  
35 40 45  
Asp Arg Ala His Tyr Asn Ile Val Thr Phe Cys Cys Lys Cys Asp Ser  
50 55 60  
Thr Leu Arg Leu Cys Val Gln Ser Thr His Val Asp Ile Arg Thr Leu  
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cat tta gag ccc caa aat gaa att ccg gtt gac ctt cta tgt cac gag 96  
His Leu Glu Pro Gln Asn Glu Ile Pro Val Asp Leu Leu Cys His Glu  
15 20 25 30  
caa tta agc gac tca gag gaa gaa aac gat gaa ata gat gga gtt aat 144  
Gln Leu Ser Asp Ser Glu Glu Glu Asn Asp Glu Ile Asp Gly Val Asn  
35 40 45

cat caa cat tta cca gcc cga cga gct gaa cca caa cgt cac aca atg 192  
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agc tca gca gac gac ctt cga gca ttc cag cag ctg ttt ctg aac acc 288  
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ctg tcc ttt gtg tgt ccg tgg tgt gca tcc cag cag ggatcc 330  
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